

EXHIBIT A:

MOUSE LKB1 COMPARED TO HUMAN LKB1

BLAST**Basic Local Alignment Search Tool**
[Edit and Resubmit](#)
[Save Search Strategies](#)
[Formatting options](#)
[Download](#)

Blast 2 sequences

SEQ ID NO: 6 (44-343) Compared to Mouse LKB1Results for: [lc|41549 SEQ ID NO: 6(433aa)]

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

lc|41549

lc|41549

Description

SEQ ID NO: 6

Molecule type

amino acid

Query Length

433

Subject ID

gl|7106425|ref|NP_035622.1|

Description

serine/threonine-protein kinase 11 [Mus musculus] >gi|81917862|sp|Q9WTK7.1|STK11_MOUSE RecName: Full=Serine/threonine-protein kinase 11;AltName: Full=Serine/threonine-protein kinase LKB1 >gi|4833595|gb|AAD31044.1|AF145287.1 Peutz-Jeghers syndrome kinase LKB1 [Mus musculus] >gi|5649101|gb|AAF21370.1|AF151711.1 protein kinase LKB1 [Mus musculus] >gi|4530575|gb|AAD22100.1|serine/threonine-protein kinase LKB1 [Mus musculus] >gi|4589404|dbj|BAAT76749.1|LKB1 [Mus musculus] >gi|5901633|gb|AAD55368.1|Peutz-Jeghers syndrome protein [Mus musculus] >gi|30851173|gb|AAH52379.1|Serine/threonine kinase 11 [Mus musculus] >gi|74186437|dbj|BAE42977.1|unnamed protein product [Mus musculus] >gi|74192527|dbj|BAE43050.1|unnamed protein product [Mus musculus] >gi|117616790|gb|ABK42413.1|Stk11 [synthetic construct] >gi|148699653|gb|EDL31600.1|serine/threonine kinase 11, isoform CRA_a [Mus musculus]

Molecule type

amino acid

Subject Length

436

ProgramBLASTP 2.2.24+ [Citation](#)**Reference**

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

Reference - compositional score matrix adjustment

Stephen F. Altschul, John C. Gish, Michael Gerz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", *FEBS J.* 272:5101-5109.

Other reports: [Search Summary](#) | [Taxonomy reports](#) | [Multiple alignment](#)[Search Parameters](#)**Search parameter name** **Search parameter value**

Program	blastp
Query range	44-343
Word size	3
Expect value	10
Hillist size	100
Gapcosts	11,1
Matrix	BLOSUM62
Low Complexity Filter	Yes
Other string	L:
Genetic Code	1
Window Size	40
Threshold	11
Composition-based stats	2

Karlin-Altschul statistics

Params **Ungapped** **Gapped**

Lambda	0.320459	0.267
K	0.139595	0.041
H	0.428592	0.14

Results Statistics**Results Statistics** **parameter name** **Results Statistics** **parameter value**

Effective search space

110297

Graphic Summary

Distribution of Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

Dot Matrix View

Plot of $|c_1|$ vs g_1 [ref|NP_035622.1| ?]

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.



Descriptions

Sequences producing significant alignments:	Score	E
	(Bits)	Value
ref NP_035523.1 serine/threonine-protein kinase 11 [Mus muscu	526	4e-154

Alignments

```

<ref>NP_035261.1 serine/threonine-protein kinase 11 [Mus musculus]
  <protein>P0WKF7.1|STTNL_MOUSE Name: Full-Serine/threonine-protein Kinase 11; AltName: Full-Serine/threonine-protein
  kinase LK81
  <db>AA031404.1|APF12487.1 Peutz-Jeghers syndrome kinase LK81 [Mus musculus]
  More sequence information...
  <db>P0WKF7.1|STTNL_MOUSE 1|APF12487.1 protein kinase LK81 [Mus musculus]
  <db>AA031404.1|APF12487.1 serine/threonine-protein kinase LK81 [Mus musculus]
  <db>AA031404.1|APF12487.1 LK81 [Mus musculus]
  <db>AA035368.1|APF12487.1 Peutz-Jeghers syndrome protein [Mus musculus]
  <db>AA035368.1|APF12487.1 STTNL [Mus musculus]
  <db>AA042977.1|APF12487.1 unnamed protein product [Mus musculus]
  <db>BA843050.1|APF12487.1 unnamed protein product [Mus musculus]
  <db>BA843050.1|APF12487.1 Sttk1 [synthetic construct]
  <db>BA843050.1|APF12487.1 Sttk1 [synthetic construct]
  <db>HDL1200.1|APF12487.1 serine/threonine kinase 11; isoform CRA_a [Mus musculus]
Length=436

Score = 526 bits (1354), Expect = 4e-154, Method: Compositional matrix adjust.
Identities = 288/300 (96%), Positives = 292/300 (98%), Gaps = 0/300 (0%)
Query 44 KLGKQYLMGQGLBGGGNGVYKVLDSLRTFLCRRAV:1|kk:kllkr1PNEAEVKKKEIQLLR 103
Sbjct 44 KLGKQYLMGQGLBGGGNGVYKVLDSLRTFLCRRAV:1|kk:kllkr1PNEAEVKKKEIQLLR 103
Query 104 RLRRHKNVQLQVVDLYNEEEKKRQKYMWMVBEYCVCQCDQBMLDLSPVEPKRPPV/CQAHGYFQLIDG 163
Sbjct 104 RLRRHKNVQLQVVDLYNEEEKKRQKYMWMVBEYCVCQCDQBMLDLSPVEPKRPPV/CQAHGYFQLIDG 163
Query 164 LEYLNSQQTIVWHDDIKPgnll11tgt:1|k1k1SISDGVVAEALHPFAAD7CTCSGSQGPAPPFPE 223
Sbjct 164 LEYLNSQQTIVWHDDIKPgnll11tgt:1|k1k1SISDGVVAEALHPFADETCRSTSGSQGPAPPFPE 223
Query 224 IANGLDTPFSQKVDFIMASGVTLLNTYTIGLYPFGEDNITYKLPEFNGKGSVAPDCCGPPLS 283
Sbjct 224 IANGLDTPFSQKVDFIMASGVTLLNTYTIGLYPFGEDNITYKLPEFNGKGSVAPDCCGPPLS 283
Query 284 DLLKQMLEYVEPAKXPSRPTQDQHSPFHPLKPKPDRPSC:1|D:D:U:TQDPRBENPVVPLIED 343
Sbjct 284 DLLKQMLEYVEPAKXPSRPTQDQHSPFHPLKPKPDRPSC:1|D:D:U:TQDPRBENPVVPLIED 343
Sbjct 284 DLLKQMLEYVEPAKXPSRPTQDQHSPFHPLKPKPDRPSC:1|D:D:U:TQDPRBENPVVPLIED 343

```

EXHIBIT B:
MULTISPECIES COMPARISON OF STRAD POLYPEPTIDE

BLAST**Basic Local Alignment Search Tool**

[Edit and Resubmit](#) [Save](#) [Search Strategies](#) [Formatting options](#) [Download](#)

Blast 2 sequences

STRAD comparison

Results for:

ref|NP_001003787.1 STE20-related kinase adapter protein alpha isoform 1 [Homo sapiens]>gi|74759034|sp|Q7RTN6.1|STRAA_...(431aa)

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

gi|51242955|ref|NP_001003787.1|
 gi|51242955|ref|NP_001003787.1|

Description

STE20-related kinase adapter protein alpha isoform 1 [Homo sapiens]>gi|74759034|sp|Q7RTN6.1|STRAA_HUMAN RecName:
Full=STE20-related kinase adapter protein alpha; Short=STRAD alpha; AltName: Full=STE20-related adapter protein; AltName:
Protein=biologically defined breast cancer antigen NY-BR-96 >gi|34494889|gb|DAA01797.1|TPA_exp; STE20-related adaptor protein
[Homo sapiens]>gi|119614691|gb|EAWv4265.1| protein kinase LYK5, isoform CRA_c [Homo sapiens]

Molecule type

amino acid

Query Length

431

Subject ID

4 subjects

Description**Molecule type**

amino acid

Subject Length

n/a

Program

BLASTP 2.2.24+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997). "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference - compositional score matrix adjustment

Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.

Other reports: [Search Summary](#) ([Taxonomy reports](#)) [\[Distance tree of results\]](#) [\[Multiple alignment\]](#)

[Search Parameters](#)

Search parameter name	Search parameter value
Program	blastp
Word size	3
Expect value	10
Hitlist size	100
Gaps/soft	11,1
Matrix	BLOSUM62
Filter string	F
Genetic Code	1
Window Size	40
Threshold	11
Composition-based stats	2

Karlin-Altschul statistics

Params	Ungapped	Gapped
--------	----------	--------

Lambda	0.318619	0.267
K	0.13404	0.041
H	0.398234	0.14

[Results Statistics](#)

Results Statistics parameter name	Results Statistics parameter value
-----------------------------------	------------------------------------

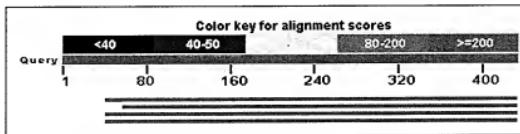
Effective search space	144800
------------------------	--------

Graphic Summary

Distribution of 4 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



Descriptions

Legend for links to other resources: UniGene GEO Gene Structure Map Viewer PubChem BioAssay
Sequences producing significant alignments:

Accession	Description	Max score	Total score	Query coverage	E value	Links
XP_850260_1	PREDICTED: similar to protein kinase LYK5 isoform 2 isoform 1 [Canis familiaris] STE20-related kinase adapter protein alpha [Bos taurus] >gi 240849230 sp EF001155306_1 STE20-related kinase adapter protein alpha [Ovis aries]>gi 240849230 sp EF001155306_1 STE20-related kinase adapter protein alpha; Short=STRADA alpha; AltName: Full=STE20-related kinase adapter protein >gi 59520179 gb AAJX08593_1 protein kinase LYK5 isoform 4 [Bos taurus]>gi 238566930 gb ACR46653_1 STRADA [Ovis aries]	786	786	90%	0.0	UGM
NP_001015603_1	STE20-related kinase adapter protein alpha [Ovis aries] >gi 296476245 gb DAA185603_1 STE20-related kinase adapter protein alpha [Ovis aries]>sp QCE69_1 STRADA_BOVIN RecName: Full=STE20-related kinase adapter protein alpha; Short=STRADA alpha; AltName: Full=STE20-related adapter protein >gi AAJX08593_1 protein kinase LYK5 isoform 4 [Bos taurus]>gi ACR46653_1 STRADA [Ovis aries]>gb DAA185603_1 STE20-related kinase adapter protein alpha [Bos taurus]	748	748	86%	0.0	UGM
NP_002402_1	STE20-related kinase adapter protein alpha [Mus musculus] >gi 128475826 gb BAB27626_1 unnamed protein product [Mus musculus] >gi 33638094 gb AAQ24157_1 protein kinase LYK5 splice variant 1 [Mus musculus]>gi 35192964 gb AAH8517_1 RIKEN cDNA 2610019A05 gene [Mus musculus]>gi 117616946 gb ABK42491_1 STLK5 [synthetic construct];>gi 123243203 emb CAM27017_1 novel protein [Mus musculus] >gi 148702203 gb ABK42491_1 protein kinase LYK5 splice variant 1 [Mus musculus]>gi 240702203 gb ABK42491_1 protein kinase LYK5 splice variant 1 [Mus musculus]>gi ABK42491_1 STLK5 [synthetic construct];>gi CAM27017_1 novel protein [Mus musculus]>gi EDL34272_1 RIKEN cDNA 2610019A05, isoform CRA_b [Mus musculus]>gi EDL34273_1 RIKEN cDNA 2610019A05, isoform CRA_b [Mus musculus]	775	775	90%	0.0	UGM
NP_877972_1	STE20-related kinase adapter protein alpha [Rattus norvegicus] >gi 1912054 sp Q7TNZ6_1 STRAA_RA RecName: Full=STE20-related kinase adapter protein alpha; Short=STRADA alpha; AltName: Full=STE20-related adapter protein >gi 33097213 gb AAP29801_1 protein kinase LYK5 [Rattus norvegicus] >gi Q7TNZ6_1 STRAA_RA RecName: Full=STE20-related kinase adapter protein alpha; Short=STRADA alpha; AltName: Full=STE20-related adapter protein >gi AAP29801_1 protein kinase LYK5 [Rattus norvegicus]	758	758	90%	0.0	UGM

Alignments

Select All Get selected sequences Distance tree of results Multiple alignment

>ref XP_850260_1 UGM PREDICTED: similar to protein kinase LYK5 isoform 2 isoform 1 [Canis familiaris] Length=394
GENE ID: 609377 STRADA STE20-related kinase adaptor alpha [Canis lupus familiaris]
Score = 786 bits (2030), Expect = 0.0, Method: Compositional matrix adjust. Identities = 376/390 (97%), Gaps = 0/390 (0%)
Query 42 TNDAESEASISFHKCEWMSPLPEPGQCYELLTVLGKPEDLMVTNLARYKPTGEVTVRR 101 Sbjct 5 TNEAESSEASISLSSKLPCEWMSPLPEPGQ YELL+IKGGKPEDLMVTNLARYKPTGEVTVRR 64
Query 102 INLEACNSNEMVTTFLQGELIVLSSKLFP-HLPN1-PYRATP ADNELWVVTSFPMWAGSKADLCT 161 INLEACNSNEMVTTFLQGELIVLSSKLFP-HLPN1-PYRATP ADNELWVVTSFPMWAGSKADLCT Sbjct 65 SHHQQRQVVRVHDPPFKYSVKWLPMWSPEVLQQLQYDQAKSDIYSVGITACELANGHVPFKD 124
Query 162 HFMDQWNLALIAAYLQLQVILKALDYIHHMGYVIRSKASHILLISVDGKVYVLSGLRSNLSMI 221 HFMDQWNLALIAAYLQLQVILKALDYIHHMGYVIRSKASHILLISUDGKVYVLSGLRSNLSMI Sbjct 125 SHHQQRQVVRVHDPPFKYSVKWLPMWSPEVLQQLQYDQAKSDIYSVGITACELANGHVPFKD 184
Query 222 SHHQQRQVVRVHDPPFKYSVKWLPMWSPEVLQQLQYDQAKSDIYSVGITACELANGHVPFKD 281 SHHQQRQVVRVHDPPFKYSVKWLPMWSPEVLQQLQYDQAKSDIYSVGITACELANGHVPFKD Sbjct 185 SHHQQRQVVRVHDPPFKYSVKWLPMWSPEVLQQLQYDQAKSDIYSVGITACELANGHVPFKD 244
Query 282 MPATQMLLEKLNGTVPCLLD-TSTIPIAEELTMSP5RSVANSGLSDSLTSTSPTPRPSNGDPS 341 MPATQMLLEKLNGTVPCLLD-TSTIPIAEELTMSTSAARNSGSDSLSLATSPTPRPSNGDPS Sbjct 245 MPATQMLLEKLNGTVPCLLD-TSTIPIAEELTMSTSAARNSGSDSLSLATSPTPRPSNGDPS 304
Query 342 HPYHRTFTSPHHHPVWQCNLPDAPRSASTLNNHSFFPKQIKRRASEALPEELLRPVPTIT 401 HPYHRTFTSPHHHPVWQCNLPDAPRSASTLNNHSFFPKQIKRRASEALPEELLRPVPTIT Sbjct 305 HPYHRTFTSPHHHPVWQCNLPDAPRSASTLNNHSFFPKQIKRRASEALPEELLRPVPTIT 364
Query 402 NFEGSQSQQSDHSG1PG1VLNTLLEEELEDDWDF 431 NFEGSQSQQSDHSG1PG1VLNTLLEEELEDDWDF

```

Sbjct 365 NFEQSQSDHSIGPFLVTLNLEELVEVDWDFE 394

>ref[NP_001015603.1] UGM STE20-related kinase adapter protein alpha [Bos taurus]
ref[NP_001153561.1] UG STE20-related kinase adapter protein alpha [Ovis aries]
sp|OP8939.1|STRA BOVIN G RecName: Full=STE20-related kinase adapter protein alpha; Short=STRADA alpha; AltName: Full=STE20-related adapter protein
gb|AAK08938.1| G protein kinase LYK5 isoform 4 [Bos taurus]
gb|ACR46653.1| G STRADA [Ovis aries]
gb|DAAL18360.1| G STE20-related kinase adapter protein alpha [Bos taurus]
Length=373

GENE ID: 515024 STRADA | STE20-related kinase adaptor alpha [Bos taurus]
(10 or fewer PubMed links)

Score = 744 bits (1932), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 356/373 (96%), Positives = 362/373 (98%), Gaps = 0/373 (0%)

Query 59 MNSFLPEPGOCYELLITVKGKFDLMTVNLRARYKPTGEYEVTVRINILEACSNEMWTFVPLQGE 118
Sbjct 1 MNSFLPEPGOCYELLITVKGKFDLMTVNLRARYKPTGEYEVTVRINILEACSNEMWTFVPLQGE 60
Query 119 LHVSKLFLPHNPWIPVPRTAIPLDNLWVTVTSFMAVGSAKDLICHTFPMCGNEILAJAYIQLG 178
Sbjct 61 LHVSKLFLPHNPWIPVPRTAIPLDNLWVTVTSFMAVGSAKDLICHTFPMCGNEILAJAYIQLG 120
Query 179 VLAJADLYTHMNGYVHRSVVAEHLVSLRGLVSKLGRSLGRSLVSHLQGKQHSGCQVWHPDPPVYSV 238
Sbjct 121 ALAKALDYIHMNGYVHRSVVAEHLVSLRGLVSKLGRSLVSHLQGKQHSGCQVWHPDPPVYSI 180
Query 239 KVLVPLMSPVELQLQNLQGDYDAKSDIYTSVGITACELANGHVPIFKDMPATQMLLEKLNGTIVPC 298
Sbjct 181 KVLVPLMSPVELQLQNLQGDYDAKSDIYTSVGITACELANGHVPIFKDMPATQMLLEKLNGTIVPC 240
Query 299 LLDTSTIPAPLTMPSFSRVSANGLSDLSLTTPRSPNGSDSPSPHYTHRTFSPFHPIHFVPP 358
Sbjct 241 LLDTSTIPAPLTMPSFSRVSANGLSDLSLTTPRSPNGSDSPSPHYTHRTFSPFHPIHFVPPVHQ 300
Query 359 CQARNDPARDASPASLTLNHSFFPKIQKRRASEALPELLRVPITPTNPFEGSQSQDHSIGPGLV 418
Sbjct 301 CQARNDPDRMFSASPASLTLNHSFFPKIQKRRASEALPELLRVPITPTNPFEGRSQSDHSIGPGLV 360
Query 419 TNLEELVEVDWDFE 431
Sbjct 361 TNLEELVEVDWDFE 373

>ref[NP_082402.1] UGM STE20-related kinase adapter protein alpha [Mus musculus]
dbj|BA276261.1| C unnamed protein product [Mus musculus]
gb|AAC24157.1| G protein kinase LYK5 splice variant 1 [Mus musculus]
gb|AAH858517.1| G RIKEN cDNA 2610019A05 gene [Mus musculus]
gb|ABK42491.1| G STLK5 [synthetic construct]
emb|CAM27017.1| G novel protein [Mus musculus]
gb|EDL34272.1| G RIKEN cDNA 2610019A05, isoform CRA_b [Mus musculus]
gb|EDL34273.1| G RIKEN cDNA 2610019A05, isoform CRA_b [Mus musculus]
Length=394

GENE ID: 72149 Strada | STE20-related kinase adaptor alpha [Mus musculus]
(Over 10 PubMed links)

Score = 775 bits (2001), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 369/390 (95%), Positives = 380/390 (98%), Gaps = 0/390 (0%)

Query 42 TNDAASSEIAPSFSKQMSVSPFLPEGCYELLITVKGKFDLMTVNLRARYKPTGEYEVTVR 101
Sbjct 5 N-ASSEASSEIAPSFSKQMSVSPFLPEGCYELLITVKGKFDLMTVNLRARYKPTGEYEVTVR 64
Query 102 INLEACSNEMWTFVPLQELVSKLFLPHNPWIPVYRATFIADELMWVTVTSFMAVGSAKDLIC 161
Sbjct 65 INLEACSNEMWTFVPLQELVSKLFLPHNPWIPVYRATFIADELMWVTVTSFMAVGSAKDLIC 124
Query 162 HFMDGNSNELAJAYIQLGVKLALDYIHMMGYVHRSVKAHSHLISVDDCKVYLSQLSNSLNSI 221
Sbjct 125 HFMDGNSNELAJAYIQLGVKLALDYIHMMGYVHRSVKAHSHLISDOKVYLSLNSLNSI 184
Query 222 SHQRQRVSPHDPPKYSVFLPVLPWSPLEQVIAQNIQGYDAKSDIYTSVGITACELANGHVPKD 281
Sbjct 185 SHQRQRVSPHDPPKYSVFLPVLPWSPLEQVIAQNIQGYDAKSDIYTSVGITACELANGHVPKD 244
Query 282 MPATMCLLEKLNLTGTVPLCLLDSTTIPAPLTMPSFSRVSANGLSDLSLTTPRSPNNSDPS 341
Sbjct 245 MPATMCLLEKLNLTGTVPLCLLDSTTIPAPLTMPSFSRVSANGLSDLSLTTPRSPNNSDPS 304
Query 342 HYPHRTSPHSPHVFHPPVQCLQRNPDRDASPASLTLNHSFFPKIQKRRASEALPELLRVPIT 401
Sbjct 305 HYPHRTSPHSPHVFHPPVQCLQRNPDRMFSASPASLTLNHSFFPKIQKRRASEALPELLRVPIT 364
Query 402 NFEQSQSDHSIGPFLVTLNLEELVEVDWDFE 431
Sbjct 365 NFEQSQSDHSIGPFLVTLNLEELVEVDWDFE 394

```

>ref|NP_877972.1| **ST20**-related kinase adapter protein alpha [Rattus norvegicus] sp|Q7TMZ6.1| STRAD RAT **C** RecName: Full-ST20-related kinase adapter protein alpha; Short-STRAD alpha; AltName: Full-ST20-related adapter protein
gb|AAP92801.1| **C** protein kinase CK2 [Rattus norvegicus]
Length=393

GENE ID: 303605 Strada | ST20-related kinase adaptor alpha [Rattus norvegicus]
(10 or fewer PubMed links)

Score = 758 bits (1958), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 362/390 (93%), Positives = 377/390 (97%), Gaps = 1/390 (0%)

Query 42	TNDASSESTASFSKQEWSFLPFGGCYELLTVIGXGFEDLMTVNLARYKPTGEYVTVRR	101
Sbjct 5	N+ASRSSTASFSK+E-MSSFLPFGGCYELL+VIGXGFEDLMTVN +RTKPTGEYVTVRR	63
Query 102	INLACCSNBMVTFLQGELHIVS KLENHNPNIIVPRATPIADNELWVVTSPFMAYGSAKDLCT	161
Sbjct 64	INLACCSNBMVTFLQGELHIVSKLFSHMNIVVPRATPIADNELWAVTSPFMAYGSAKDLCT	123
Query 162	HFMGDMNELAIAJAYILOQVILKALDYIHMHGYVHRSVKASHILISVGKVYLSGLRSNLSMI	221
Sbjct 124	HFMGDM+ELAIAJAYILOQVILKALDYIHMHGYVHRSVKASHILIS DGKVYVLSGLRSNLSMI	183
Query 222	SHQORQRVHDPPKYSVKVLPMWSPEVQLQNLQGYDAKSDIYSVGIIACELANGHVPFKD	281
Sbjct 184	SHQORQRAVHDPPKYSIKVLPMWSPEVQLQNLQGYDAKSDIYSVGIIACELANGHVPFKD	243
Query 282	MPATCMLLEKLNGTVPCLLDTSTI ^P AEEBLTMSPERSVANSCLSLDSLITSTTRPSNGDPS	341
Sbjct 244	MPATCMLLEKLNGTVPCLLDTSTI ^P AEEBLTMSPERSIANPGLNDSLAAAGSLRPANGDPS	303
Query 342	HPYHRTFTSPMHHIFVBCQCLQRNPDPARPSASTILNHSPFKQIKKRASEALPELLRPVTPIT	401
Sbjct 304	HPYHRTFTSPMHHNFVBCQCLQRNPDPARPNASTILNHSSFFKQIKKRASEALPELLRPVTPIT	363
Query 402	NFBGQSQQHNSGICPGLVTLNLERLEVDDWEF	431
Sbjct 364	+FEGGSQSQQHNSGICPGLVTLNLERLEVDDWEF	393

Select All [Get selected sequences](#) [Distance tree](#) of results [Multiple alignment](#)

EXHIBIT C:
MULTISPECIES COMPARISON OF MO25 POLYPEPTIDE

NCBI

All Databases PubMed Nucleotide Protein Genome Structure OMIM PMC Journals Books

Search [HomoloGene] for Go Clear

Limits Preview/Index History Clipboard Details

Display Alignment Scores Show 20 Send to

All: 1 Fungi: 0 Mammals: 0

Γ 1: HomoloGene-69212. Gene conserved in Eukaryota

Download , Links

Pairwise Alignment Scores

Species	Gene	Identity (%)		Substitution Rates ¹			Blast
		Symbol	Protein	DNA	d	d_N/d_S	
Homo sapiens	CAB39						
vs. <i>Pan troglodytes</i>	CAB39	100.0	99.9	0.001	0	0	Blast
vs. <i>Canis lupus familiaris</i>	CAB39	99.4	94.8	0.054	0	0	Blast
vs. <i>Bos taurus</i>	CAB39	100.0	94.0	0.062	0	0	Blast
vs. <i>Mus musculus</i>	Cab39	98.8	92.4	0.080	0	0	Blast
vs. <i>Rattus norvegicus</i>	Cab39	99.4	92.6	0.078	0	0	Blast
vs. <i>Danio rerio</i>	cab39	93.0	79.6	0.239	0	0	Blast
vs. <i>Drosophila melanogaster</i>	Mo25	71.9	63.8	0.494	0	0	Blast
vs. <i>Anopheles gambiae</i>	AgaP_AGAP000812	72.6	64.1	0.489	0	0	Blast
vs. <i>Anopheles gambiae</i>	AgaP_AGAP011060	73.3	64.8	0.476	0	0	Blast
vs. <i>Caenorhabditis elegans</i>	mop-25.1	65.3	61.7	0.537	0	0	Blast
vs. <i>Caenorhabditis elegans</i>	mop-25.2	61.2	60.5	0.561	0	0	Blast
vs. <i>Schizosaccharomyces pombe</i>	pmo25	51.7	55.7	0.669	0	0	Blast
vs. <i>Arabidopsis thaliana</i>	AT4G17270	44.7	52.4	0.756	0	0	Blast
vs. <i>Arabidopsis thaliana</i>	AT5G47540	43.5	52.5	0.753	0	0	Blast
vs. <i>Oryza sativa</i>	Os07g0585100	47.0	54.1	0.711	0	0	Blast
Pan troglodytes	CAB39						
vs. <i>Homo sapiens</i>	CAB39	100.0	99.9	0.001	0	0	Blast
vs. <i>Canis lupus familiaris</i>	CAB39	99.4	94.8	0.054	0	0	Blast
vs. <i>Bos taurus</i>	CAB39	100.0	93.9	0.063	0	0	Blast
vs. <i>Mus musculus</i>	Cab39	98.8	92.3	0.081	0	0	Blast
vs. <i>Rattus norvegicus</i>	Cab39	99.4	92.5	0.079	0	0	Blast
vs. <i>Danio rerio</i>	cab39	93.0	79.6	0.239	0	0	Blast
vs. <i>Drosophila melanogaster</i>	Mo25	71.9	63.8	0.494	0	0	Blast
vs. <i>Anopheles gambiae</i>	AgaP_AGAP000812	72.6	64.1	0.489	0	0	Blast
vs. <i>Anopheles gambiae</i>	AgaP_AGAP011060	73.3	64.8	0.476	0	0	Blast
vs. <i>Caenorhabditis elegans</i>	mop-25.1	65.3	61.7	0.537	0	0	Blast
vs. <i>Caenorhabditis elegans</i>	mop-25.2	61.2	60.5	0.561	0	0	Blast
vs. <i>Schizosaccharomyces pombe</i>	pmo25	51.7	55.6	0.672	0	0	Blast
vs. <i>Arabidopsis thaliana</i>	AT4G17270	44.7	52.4	0.756	0	0	Blast
vs. <i>Arabidopsis thaliana</i>	AT5G47540	43.5	52.5	0.753	0	0	Blast
vs. <i>Oryza sativa</i>	Os07g0585100	47.0	54.1	0.711	0	0	Blast
Canis lupus familiaris	CAB39						
vs. <i>Homo sapiens</i>	CAB39	99.4	94.8	0.054	0	0	Blast
vs. <i>Pan troglodytes</i>	CAB39	99.4	94.8	0.054	0	0	Blast
vs. <i>Bos taurus</i>	CAB39	99.4	93.5	0.067	0	0	Blast
vs. <i>Mus musculus</i>	Cab39	98.8	91.2	0.094	0	0	Blast

vs. <i>Rattus norvegicus</i>	Cab39	99.4	91.4	0.091	0	0	Blast
vs. <i>Danio rerio</i>	cab39	93.0	79.6	0.239	0	0	Blast
vs. <i>Drosophila melanogaster</i>	Mo25	72.5	64.5	0.480	0	0	Blast
vs. <i>Anopheles gambiae</i>	AgaP_AGAP000812	72.9	64.5	0.482	0	0	Blast
vs. <i>Anopheles gambiae</i>	AgaP_AGAP011060	73.6	64.9	0.474	0	0	Blast
vs. <i>Caenorhabditis elegans</i>	mop-25.1	65.3	61.1	0.549	0	0	Blast
vs. <i>Caenorhabditis elegans</i>	mop-25.2	60.9	60.3	0.565	0	0	Blast
vs. <i>Schizosaccharomyces pombe</i>	pmo25	51.7	54.5	0.700	0	0	Blast
vs. <i>Arabidopsis thaliana</i>	AT4G17270	44.7	52.1	0.764	0	0	Blast
vs. <i>Arabidopsis thaliana</i>	AT5G47540	43.5	52.1	0.764	0	0	Blast
vs. <i>Oryza sativa</i>	Os07g0585100	47.0	54.1	0.711	0	0	Blast
<i>Bos taurus</i>	CAB39						
vs. <i>Homo sapiens</i>	CAB39	100.0	94.0	0.062	0	0	Blast
vs. <i>Pan troglodytes</i>	CAB39	100.0	93.9	0.063	0	0	Blast
vs. <i>Canis lupus familiaris</i>	CAB39	99.4	93.5	0.067	0	0	Blast
vs. <i>Mus musculus</i>	Cab39	98.8	91.6	0.089	0	0	Blast
vs. <i>Rattus norvegicus</i>	Cab39	99.4	92.0	0.085	0	0	Blast
vs. <i>Danio rerio</i>	cab39	93.0	79.4	0.241	0	0	Blast
vs. <i>Drosophila melanogaster</i>	Mo25	71.9	65.7	0.458	0	0	Blast
vs. <i>Anopheles gambiae</i>	AgaP_AGAP000812	72.6	65.4	0.465	0	0	Blast
vs. <i>Anopheles gambiae</i>	AgaP_AGAP011060	73.3	66.2	0.450	0	0	Blast
vs. <i>Caenorhabditis elegans</i>	mop-25.1	65.3	61.7	0.537	0	0	Blast
vs. <i>Caenorhabditis elegans</i>	mop-25.2	61.2	60.6	0.559	0	0	Blast
vs. <i>Schizosaccharomyces pombe</i>	pmo25	51.7	53.8	0.718	0	0	Blast
vs. <i>Arabidopsis thaliana</i>	AT4G17270	44.7	52.1	0.764	0	0	Blast
vs. <i>Arabidopsis thaliana</i>	AT5G47540	43.5	52.5	0.753	0	0	Blast
vs. <i>Oryza sativa</i>	Os07g0585100	47.0	54.5	0.701	0	0	Blast
<i>Mus musculus</i>	Cab39						
vs. <i>Homo sapiens</i>	CAB39	98.8	92.4	0.080	0	0	Blast
vs. <i>Pan troglodytes</i>	CAB39	98.8	92.3	0.081	0	0	Blast
vs. <i>Canis lupus familiaris</i>	CAB39	98.8	91.2	0.094	0	0	Blast
vs. <i>Bos taurus</i>	CAB39	98.8	91.6	0.089	0	0	Blast
vs. <i>Rattus norvegicus</i>	Cab39	99.4	96.4	0.037	0	0	Blast
vs. <i>Danio rerio</i>	cab39	92.4	80.4	0.227	0	0	Blast
vs. <i>Drosophila melanogaster</i>	Mo25	72.2	66.5	0.445	0	0	Blast
vs. <i>Anopheles gambiae</i>	AgaP_AGAP000812	72.9	66.4	0.446	0	0	Blast
vs. <i>Anopheles gambiae</i>	AgaP_AGAP011060	72.6	66.6	0.443	0	0	Blast
vs. <i>Caenorhabditis elegans</i>	mop-25.1	64.3	61.4	0.543	0	0	Blast
vs. <i>Caenorhabditis elegans</i>	mop-25.2	61.2	59.6	0.580	0	0	Blast
vs. <i>Schizosaccharomyces pombe</i>	pmo25	51.7	54.0	0.713	0	0	Blast
vs. <i>Arabidopsis thaliana</i>	AT4G17270	45.0	53.1	0.737	0	0	Blast
vs. <i>Arabidopsis thaliana</i>	AT5G47540	43.5	51.7	0.775	0	0	Blast
vs. <i>Oryza sativa</i>	Os07g0585100	47.0	53.9	0.716	0	0	Blast
<i>Rattus norvegicus</i>	Cab39						
vs. <i>Homo sapiens</i>	CAB39	99.4	92.6	0.078	0	0	Blast
vs. <i>Pan troglodytes</i>	CAB39	99.4	92.5	0.079	0	0	Blast
vs. <i>Canis lupus familiaris</i>	CAB39	99.4	91.4	0.091	0	0	Blast
vs. <i>Bos taurus</i>	CAB39	99.4	92.0	0.085	0	0	Blast
vs. <i>Mus musculus</i>	Cab39	99.4	96.4	0.037	0	0	Blast
vs. <i>Danio rerio</i>	cab39	93.0	80.0	0.233	0	0	Blast
vs. <i>Drosophila melanogaster</i>	Mo25	72.2	65.7	0.458	0	0	Blast
vs. <i>Anopheles gambiae</i>	AgaP_AGAP000812	72.9	66.0	0.454	0	0	Blast

vs. <i>Anopheles gambiae</i>	AgaP_AGAP011060	72.6	65.9	0.455	0	0	Blast
vs. <i>Caenorhabditis elegans</i>	mop-25.1	64.3	61.2	0.547	0	0	Blast
vs. <i>Caenorhabditis elegans</i>	mop-25.2	61.2	59.8	0.576	0	0	Blast
vs. <i>Schizosaccharomyces pombe</i>	pmo25	51.7	53.7	0.720	0	0	Blast
vs. <i>Arabidopsis thaliana</i>	AT4G17270	44.7	52.2	0.761	0	0	Blast
vs. <i>Arabidopsis thaliana</i>	AT5G47540	43.5	51.5	0.781	0	0	Blast
vs. <i>Oryza sativa</i>	Os07g0585100	47.0	54.2	0.708	0	0	Blast
Danio rerio	cab39						
vs. <i>Homo sapiens</i>	CAB39	93.0	79.6	0.239	0	0	Blast
vs. <i>Pan troglodytes</i>	CAB39	93.0	79.6	0.239	0	0	Blast
vs. <i>Canis lupus familiaris</i>	CAB39	93.0	79.6	0.239	0	0	Blast
vs. <i>Bos taurus</i>	CAB39	93.0	79.4	0.241	0	0	Blast
vs. <i>Mus musculus</i>	Cab39	92.4	80.4	0.227	0	0	Blast
vs. <i>Rattus norvegicus</i>	Cab39	93.0	80.0	0.233	0	0	Blast
vs. <i>Drosophila melanogaster</i>	Mo25	69.5	68.8	0.404	0	0	Blast
vs. <i>Anopheles gambiae</i>	AgaP_AGAP000812	70.9	69.4	0.393	0	0	Blast
vs. <i>Anopheles gambiae</i>	AgaP_AGAP011060	70.6	67.8	0.421	0	0	Blast
vs. <i>Caenorhabditis elegans</i>	mop-25.1	63.8	62.1	0.529	0	0	Blast
vs. <i>Caenorhabditis elegans</i>	mop-25.2	60.9	61.1	0.548	0	0	Blast
vs. <i>Schizosaccharomyces pombe</i>	pmo25	51.7	52.5	0.753	0	0	Blast
vs. <i>Arabidopsis thaliana</i>	AT4G17270	45.3	53.2	0.734	0	0	Blast
vs. <i>Arabidopsis thaliana</i>	AT5G47540	43.8	52.1	0.764	0	0	Blast
vs. <i>Oryza sativa</i>	Os07g0585100	47.0	53.7	0.722	0	0	Blast
Drosophila melanogaster	Mo25						
vs. <i>Homo sapiens</i>	CAB39	71.9	63.8	0.494	0	0	Blast
vs. <i>Pan troglodytes</i>	CAB39	71.9	63.8	0.494	0	0	Blast
vs. <i>Canis lupus familiaris</i>	CAB39	72.5	64.5	0.480	0	0	Blast
vs. <i>Bos taurus</i>	CAB39	71.9	65.7	0.458	0	0	Blast
vs. <i>Mus musculus</i>	Cab39	72.2	66.5	0.445	0	0	Blast
vs. <i>Rattus norvegicus</i>	Cab39	72.2	65.7	0.458	0	0	Blast
vs. <i>Danio rerio</i>	cab39	69.5	68.8	0.404	0	0	Blast
vs. <i>Anopheles gambiae</i>	AgaP_AGAP000812	88.7	82.2	0.203	0	0	Blast
vs. <i>Anopheles gambiae</i>	AgaP_AGAP011060	86.4	82.5	0.199	0	0	Blast
vs. <i>Caenorhabditis elegans</i>	mop-25.1	65.8	64.3	0.485	0	0	Blast
vs. <i>Caenorhabditis elegans</i>	mop-25.2	63.5	59.8	0.576	0	0	Blast
vs. <i>Schizosaccharomyces pombe</i>	pmo25	52.1	51.1	0.791	0	0	Blast
vs. <i>Arabidopsis thaliana</i>	AT4G17270	42.4	51.3	0.785	0	0	Blast
vs. <i>Arabidopsis thaliana</i>	AT5G47540	42.1	50.2	0.818	0	0	Blast
vs. <i>Oryza sativa</i>	Os07g0585100	46.2	52.3	0.758	0	0	Blast
Anopheles gambiae	AgaP_AGAP000812						
vs. <i>Homo sapiens</i>	CAB39	72.6	64.1	0.489	0	0	Blast
vs. <i>Pan troglodytes</i>	CAB39	72.6	64.1	0.489	0	0	Blast
vs. <i>Canis lupus familiaris</i>	CAB39	72.9	64.5	0.482	0	0	Blast
vs. <i>Bos taurus</i>	CAB39	72.6	65.4	0.465	0	0	Blast
vs. <i>Mus musculus</i>	Cab39	72.9	66.4	0.446	0	0	Blast
vs. <i>Rattus norvegicus</i>	Cab39	72.9	66.0	0.454	0	0	Blast
vs. <i>Danio rerio</i>	cab39	70.9	69.4	0.393	0	0	Blast
vs. <i>Drosophila melanogaster</i>	Mo25	88.7	82.2	0.203	0	0	Blast
vs. <i>Anopheles gambiae</i>	AgaP_AGAP011060	93.7	90.7	0.100	0	0	Blast
vs. <i>Caenorhabditis elegans</i>	mop-25.1	66.2	64.9	0.474	0	0	Blast
vs. <i>Caenorhabditis elegans</i>	mop-25.2	62.0	61.8	0.534	0	0	Blast
vs. <i>Schizosaccharomyces pombe</i>	pmo25	50.9	50.1	0.821	0	0	Blast

vs. <i>Arabidopsis thaliana</i>	AT4G17270	43.1	51.1	0.793	0	0	Blast
vs. <i>Arabidopsis thaliana</i>	AT5G47540	43.3	49.8	0.830	0	0	Blast
vs. <i>Oryza sativa</i>	Os07g0585100	46.0	51.6	0.776	0	0	Blast
Anopheles gambiae	AgaP_AGAP011060						
vs. <i>Homo sapiens</i>	CAB39	73.3	64.8	0.476	0	0	Blast
vs. <i>Pan troglodytes</i>	CAB39	73.3	64.8	0.476	0	0	Blast
vs. <i>Canis lupus familiaris</i>	CAB39	73.6	64.9	0.474	0	0	Blast
vs. <i>Bos taurus</i>	CAB39	73.3	66.2	0.450	0	0	Blast
vs. <i>Mus musculus</i>	Cab39	72.6	66.6	0.443	0	0	Blast
vs. <i>Rattus norvegicus</i>	Cab39	72.6	65.9	0.455	0	0	Blast
vs. <i>Danio rerio</i>	cab39	70.6	67.8	0.421	0	0	Blast
vs. <i>Drosophila melanogaster</i>	Mo25	86.4	82.5	0.199	0	0	Blast
vs. <i>Anopheles gambiae</i>	AgaP_AGAP000812	93.7	90.7	0.100	0	0	Blast
vs. <i>Caenorhabditis elegans</i>	mop-25.1	63.5	65.4	0.464	0	0	Blast
vs. <i>Caenorhabditis elegans</i>	mop-25.2	60.5	60.5	0.561	0	0	Blast
vs. <i>Schizosaccharomyces pombe</i>	pmo25	50.6	50.0	0.824	0	0	Blast
vs. <i>Arabidopsis thaliana</i>	AT4G17270	43.1	50.6	0.807	0	0	Blast
vs. <i>Arabidopsis thaliana</i>	AT5G47540	42.9	48.5	0.869	0	0	Blast
vs. <i>Oryza sativa</i>	Os07g0585100	44.8	50.8	0.800	0	0	Blast
Caenorhabditis elegans	mop-25.1						
vs. <i>Homo sapiens</i>	CAB39	65.3	61.7	0.537	0	0	Blast
vs. <i>Pan troglodytes</i>	CAB39	65.3	61.7	0.537	0	0	Blast
vs. <i>Canis lupus familiaris</i>	CAB39	65.3	61.1	0.549	0	0	Blast
vs. <i>Bos taurus</i>	CAB39	65.3	61.7	0.537	0	0	Blast
vs. <i>Mus musculus</i>	Cab39	64.3	61.4	0.543	0	0	Blast
vs. <i>Rattus norvegicus</i>	Cab39	64.3	61.2	0.547	0	0	Blast
vs. <i>Danio rerio</i>	cab39	63.8	62.1	0.529	0	0	Blast
vs. <i>Drosophila melanogaster</i>	Mo25	65.8	64.3	0.485	0	0	Blast
vs. <i>Anopheles gambiae</i>	AgaP_AGAP000812	66.2	64.9	0.474	0	0	Blast
vs. <i>Anopheles gambiae</i>	AgaP_AGAP011060	63.5	65.4	0.464	0	0	Blast
vs. <i>Caenorhabditis elegans</i>	mop-25.2	72.1	66.2	0.450	0	0	Blast
vs. <i>Schizosaccharomyces pombe</i>	pmo25	51.7	53.3	0.731	0	0	Blast
vs. <i>Arabidopsis thaliana</i>	AT4G17270	45.5	50.8	0.800	0	0	Blast
vs. <i>Arabidopsis thaliana</i>	AT5G47540	46.5	50.1	0.822	0	0	Blast
vs. <i>Oryza sativa</i>	Os07g0585100	48.5	52.7	0.747	0	0	Blast
Caenorhabditis elegans	mop-25.2						
vs. <i>Homo sapiens</i>	CAB39	61.2	60.5	0.561	0	0	Blast
vs. <i>Pan troglodytes</i>	CAB39	61.2	60.5	0.561	0	0	Blast
vs. <i>Canis lupus familiaris</i>	CAB39	60.9	60.3	0.565	0	0	Blast
vs. <i>Bos taurus</i>	CAB39	61.2	60.6	0.559	0	0	Blast
vs. <i>Mus musculus</i>	Cab39	61.2	59.6	0.580	0	0	Blast
vs. <i>Rattus norvegicus</i>	Cab39	61.2	59.8	0.576	0	0	Blast
vs. <i>Danio rerio</i>	cab39	60.9	61.1	0.548	0	0	Blast
vs. <i>Drosophila melanogaster</i>	Mo25	63.5	59.8	0.576	0	0	Blast
vs. <i>Anopheles gambiae</i>	AgaP_AGAP000812	62.0	61.8	0.534	0	0	Blast
vs. <i>Anopheles gambiae</i>	AgaP_AGAP011060	60.5	60.5	0.561	0	0	Blast
vs. <i>Caenorhabditis elegans</i>	mop-25.1	72.1	66.2	0.450	0	0	Blast
vs. <i>Schizosaccharomyces pombe</i>	pmo25	48.8	52.0	0.765	0	0	Blast
vs. <i>Arabidopsis thaliana</i>	AT4G17270	42.9	49.5	0.839	0	0	Blast
vs. <i>Arabidopsis thaliana</i>	AT5G47540	42.2	49.9	0.827	0	0	Blast
vs. <i>Oryza sativa</i>	Os07g0585100	45.5	51.2	0.789	0	0	Blast
Schizosaccharomyces pombe	pmo25						

vs. <i>Homo sapiens</i>	CAB39	51.7	55.7	0.669	0	0	Blast
vs. <i>Pan troglodytes</i>	CAB39	51.7	55.6	0.672	0	0	Blast
vs. <i>Canis lupus familiaris</i>	CAB39	51.7	54.5	0.700	0	0	Blast
vs. <i>Bos taurus</i>	CAB39	51.7	53.8	0.718	0	0	Blast
vs. <i>Mus musculus</i>	Cab39	51.7	54.0	0.713	0	0	Blast
vs. <i>Rattus norvegicus</i>	Cab39	51.7	53.7	0.720	0	0	Blast
vs. <i>Danio rerio</i>	cab39	51.7	52.5	0.753	0	0	Blast
vs. <i>Drosophila melanogaster</i>	Mo25	52.1	51.1	0.791	0	0	Blast
vs. <i>Anopheles gambiae</i>	AgaP_AGAP000812	50.9	50.1	0.821	0	0	Blast
vs. <i>Anopheles gambiae</i>	AgaP_AGAP011060	50.6	50.0	0.824	0	0	Blast
vs. <i>Caenorhabditis elegans</i>	mop-25.1	51.7	53.3	0.731	0	0	Blast
vs. <i>Caenorhabditis elegans</i>	mop-25.2	48.8	52.0	0.765	0	0	Blast
vs. <i>Arabidopsis thaliana</i>	AT4G17270	39.9	51.0	0.794	0	0	Blast
vs. <i>Arabidopsis thaliana</i>	AT5G47540	40.4	50.3	0.816	0	0	Blast
vs. <i>Oryza sativa</i>	Os07g0585100	43.0	51.4	0.782	0	0	Blast
Arabidopsis thaliana	AT4G17270						
vs. <i>Homo sapiens</i>	CAB39	44.7	52.4	0.756	0	0	Blast
vs. <i>Pan troglodytes</i>	CAB39	44.7	52.4	0.756	0	0	Blast
vs. <i>Canis lupus familiaris</i>	CAB39	44.7	52.1	0.764	0	0	Blast
vs. <i>Bos taurus</i>	CAB39	44.7	52.1	0.764	0	0	Blast
vs. <i>Mus musculus</i>	Cab39	45.0	53.1	0.737	0	0	Blast
vs. <i>Rattus norvegicus</i>	Cab39	44.7	52.2	0.761	0	0	Blast
vs. <i>Danio rerio</i>	cab39	45.3	53.2	0.734	0	0	Blast
vs. <i>Drosophila melanogaster</i>	Mo25	42.4	51.3	0.785	0	0	Blast
vs. <i>Anopheles gambiae</i>	AgaP_AGAP000812	43.1	51.1	0.793	0	0	Blast
vs. <i>Anopheles gambiae</i>	AgaP_AGAP011060	43.1	50.6	0.807	0	0	Blast
vs. <i>Caenorhabditis elegans</i>	mop-25.1	45.5	50.8	0.800	0	0	Blast
vs. <i>Caenorhabditis elegans</i>	mop-25.2	42.9	49.5	0.839	0	0	Blast
vs. <i>Schizosaccharomyces pombe</i>	pmo25	39.9	51.0	0.794	0	0	Blast
vs. <i>Arabidopsis thaliana</i>	AT5G47540	87.2	85.4	0.162	0	0	Blast
vs. <i>Oryza sativa</i>	Os07g0585100	70.8	70.5	0.374	0	0	Blast
Arabidopsis thaliana	AT5G47540						
vs. <i>Homo sapiens</i>	CAB39	43.5	52.5	0.753	0	0	Blast
vs. <i>Pan troglodytes</i>	CAB39	43.5	52.5	0.753	0	0	Blast
vs. <i>Canis lupus familiaris</i>	CAB39	43.5	52.1	0.764	0	0	Blast
vs. <i>Bos taurus</i>	CAB39	43.5	52.5	0.753	0	0	Blast
vs. <i>Mus musculus</i>	Cab39	43.5	51.7	0.775	0	0	Blast
vs. <i>Rattus norvegicus</i>	Cab39	43.5	51.5	0.781	0	0	Blast
vs. <i>Danio rerio</i>	cab39	43.8	52.1	0.764	0	0	Blast
vs. <i>Drosophila melanogaster</i>	Mo25	42.1	50.2	0.818	0	0	Blast
vs. <i>Anopheles gambiae</i>	AgaP_AGAP000812	43.3	49.8	0.830	0	0	Blast
vs. <i>Anopheles gambiae</i>	AgaP_AGAP011060	42.9	48.5	0.869	0	0	Blast
vs. <i>Caenorhabditis elegans</i>	mop-25.1	46.5	50.1	0.822	0	0	Blast
vs. <i>Caenorhabditis elegans</i>	mop-25.2	42.2	49.9	0.827	0	0	Blast
vs. <i>Schizosaccharomyces pombe</i>	pmo25	40.4	50.3	0.816	0	0	Blast
vs. <i>Arabidopsis thaliana</i>	AT4G17270	87.2	85.4	0.162	0	0	Blast
vs. <i>Oryza sativa</i>	Os07g0585100	76.5	72.1	0.349	0	0	Blast
Oryza sativa	Os07g0585100						
vs. <i>Homo sapiens</i>	CAB39	47.0	54.1	0.711	0	0	Blast
vs. <i>Pan troglodytes</i>	CAB39	47.0	54.1	0.711	0	0	Blast
vs. <i>Canis lupus familiaris</i>	CAB39	47.0	54.1	0.711	0	0	Blast
vs. <i>Bos taurus</i>	CAB39	47.0	54.5	0.701	0	0	Blast

vs. <i>Mus musculus</i>	Cab39	47.0	53.9	0.716	0	0	Blast
vs. <i>Rattus norvegicus</i>	Cab39	47.0	54.2	0.708	0	0	Blast
vs. <i>Danio rerio</i>	cab39	47.0	53.7	0.722	0	0	Blast
vs. <i>Drosophila melanogaster</i>	Mo25	46.2	52.3	0.758	0	0	Blast
vs. <i>Anopheles gambiae</i>	AgaP_ AGAP000812	46.0	51.6	0.776	0	0	Blast
vs. <i>Anopheles gambiae</i>	AgaP_ AGAP011060	44.8	50.8	0.800	0	0	Blast
vs. <i>Caenorhabditis elegans</i>	mop-25.1	48.5	52.7	0.747	0	0	Blast
vs. <i>Caenorhabditis elegans</i>	mop-25.2	45.5	51.2	0.789	0	0	Blast
vs. <i>Schizosaccharomyces pombe</i>	pmo25	43.0	51.4	0.782	0	0	Blast
vs. <i>Arabidopsis thaliana</i>	AT4G17270	70.8	70.5	0.374	0	0	Blast
vs. <i>Arabidopsis thaliana</i>	AT5G47540	76.5	72.1	0.349	0	0	Blast

[†] We present three rates for nucleotide substitutions per site, as defined below:

- d: the number of nucleotide substitutions per site, corrected for multiple substitutions using the method of Jukes and Cantor (1969).
- d_N/d_S : the ratio of the rate of nonsynonymous substitutions (d_N) to the rate of synonymous substitutions(d_S), calculated using the method of Nei and Gojobori (1986). A high value of this metric indicates adaptive selection, whereas a low value indicates purifying selection.
- d_{NR}/d_{NC} : the ratio of radical nonsynonymous substitutions (d_{NR}) to conservative nonsynonymous substitutions (d_{NC}), calculated using the method of Hughes et al. (1990). This metric is analogous to d_N/d_S , but it has the advantage of being useful for studying the evolution of sequences that diverged in the distant past.

References

- Jukes TH, Cantor CR. Evolution of protein molecules. In: HN Munro, editor. Mammalian protein metabolism III. New York: Academic Press; 1969. p.21-132.
- Nei M, Gojobori T. Simple methods for estimating the numbers of synonymous and nonsynonymous nucleotide substitutions. Mol Biol Evol. 1986;3(5):418-26.
- Hughes AL, Ota T, Nei M. Positive Darwinian selection promotes charge profile diversity in the antigen-binding cleft of class I MHC molecules. Mol Biol Evol. 1990;7(6):515-24.

Display Show Send to

[Write to the Help Desk](#)

[NCBI](#) | [NLM](#) | [NIH](#)

[Department of Health & Human Services](#)

[Privacy Statement](#) | [Freedom of Information Act](#) | [Disclaimer](#)

EXHIBIT D:
COMPARISON OF RAT AND HUMAN LKB1

BLAST**Basic Local Alignment Search Tool**

[Edit and Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download](#)

Blast 2 sequences

SEQ ID NO: 6

Results for: SEQ ID NO: 6(433aa) ▾

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID**Description**

SEQ ID NO: 6

Molecule type

amino acid

Query Length

433

Subject ID**Description**

serine/threonine-protein kinase 11 [Rattus norvegicus] > serine/threonine kinase 11 (predicted), isoform CRA_a [Rattus norvegicus]

Molecule type

amino acid

Subject Length

436

Program

BLASTP 2.2.24+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

Reference - compositional score matrix adjustment

Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", *FEBS J.* 272:5101-5109.

Other reports: [Search Summary](#) [\[Taxonomy reports\]](#) [\[Multiple alignment\]](#)

[Search Parameters](#)

Search parameter name **Search parameter value**

Program	blastp
Query range	44-343
Word size	3
Expect value	10
Hitlist size	100
Gapcosts	11,1
Matrix	BLOSUM62

Low Complexity Filter	Yes
Filter string	L;
Genetic Code	1
Window Size	40
Threshold	11
Composition-based stats	2

Karlin-Altschul statistics

Params	Ungapped	Gapped
--------	----------	--------

Lambda	0.320459	0.267
K	0.139595	0.041
H	0.429592	0.14

Results Statistics

Results	Statistics parameter name	Results	Statistics parameter value
---------	---------------------------	---------	----------------------------

Effective search space	110297
------------------------	--------

Graphic Summary

Distribution of Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

Dot Matrix View**Plot of Icl|17777 vs gi|157820995|ref|NP_001101539.1| [?]**

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.

**Descriptions**

		Score (Bits)	E Value
Sequences producing significant alignments:			
<u>ref NP_001101539.1 </u> serine/threonine-protein kinase 11 [Rattus norvegicus]	525	1e-153	

Alignments

>ref|NP_001101539.1| serine/threonine-protein kinase 11 [Rattus norvegicus]
 gb|EDL8933.1| serine/threonine kinase 11 (predicted), isoform CRA_a [Rattus norvegicus]
 Length=436

Score = 525 bits (1351), Expect = 1e-153, Method: Compositional matrix adjust.
Identities = 287/300 (96%), Positives = 291/300 (97%), Gaps = 0/300 (0%)
Query 44 KLIGKYLMDGLLGEGSYGVKEVLDSETLCRRRAVKilkkkklrrriPNGEANVKEIQLLR 103
Sbjct 44 KLIGKYLMDGLLGEGSYGVKEVLDSETLCRRRAVKILKKKKLRRIPNGEANVKEIQLLR 103
Query 104 RLRHKNVIQLVDVLYNEEKQKMYMVMMEYCVCGQMQLDSLVPPEKRFPVCQAHGYFCQLIDG 163
RLRH+NVIQLVDVLYNEEKQKMYMVMMEYCVCGQMQLDSLVPPEKRFPVCQAHGYF QLIDG 163
Sbjct 104 RLRRHNVIQLVDVLYNEEKQKMYMVMMEYCVCGQMQLDSLVPPEKRFPVCQAHGYF RQLIDG 163
Query 164 LEYLHSQGIVVKDIKPgnlllttgg1kISDLGVAAEALHPFAADDTCRTSQGSPAFQPPE 223
LEYLHSQGIVVKDIKPgnlllTT GTLKTSSDLGVAAEALHPFA DDTCRTSQGSPAFQPPE 223
Sbjct 164 LEYLHSQGIVVKDIKPgnlllTTGTNLTKISDLGVAAEALHPFAVDDTCRTSQGSPAFQPPE 223
Query 224 IANGLDTFSQFKVUDIMSAQVTLYNITTGlyPFEGDNiYKLPENiG+ II DC PPLS 283
IANGLDTFSQFKVUDIMSAQVTLYNITTGlyPFEGDNiYKLPENiG+ II DC PPLS 283
Sbjct 224 IANGLDTFSQFKVUDIMSAQVTLYNITTGlyPFEGDNiYKLPENiGGRGDTTIPCDCAPLS 283
Query 284 DLLKGMLYEPAKRFSSIRQIQRHSWFRKKHppaceapvpipospDTKDRWRSMTVVPYLED 343
DLL+GMLYEPAKRFSSIRQIQRHSWFRKKH AEA VPIPSPDTKDRWRSMTVVPYLED 343
Sbjct 284 DLLRGMLYEPAKRFSSIRQIQRHSWFRKKHPLAEALVPIPPSPDTKDRWRSMTVVPYLED 343